(1) GENERAL INFORMATION:

(i) APPLICANTS: Boon, Thierry, Van den Eynde, Benoît

(ii) TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor Rejection Antigens and Uses Thereof

(iii) NUMBER OF SEQUENCES: 16

(iv) CORRESPONDENCE ADDRESS:
     (A) ADDRESSEE: Felfe & Lynch
     (B) STREET: 805 Third Avenue
     (C) CITY: New York City
     (D) STATE: New York
     (F) ZIP: 10022

(v) COMPUTER READABLE FORM:
     (A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
     (B) COMPUTER: IBM
     (C) OPERATING SYSTEM: PC-DOS
     (D) SOFTWARE: Wordperfect

(vi) CURRENT APPLICATION DATA:
     (A) APPLICATION NUMBER: 07/807,043
     (B) FILING DATE: 12-DECEMBER-1991
     (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
     (A) APPLICATION NUMBER: 07/764,364
     (B) FILING DATE: 23-SEPTEMBER-1991

(vii) PRIOR APPLICATION DATA:
     (A) APPLICATION NUMBER: 07/728,838
     (b) FILING DATE: 9-JULY-1991

(vii) PRIOR APPLICATION DATA:
     (A) APPLICATION NUMBER: 07/705,702
     (B) FILING DATE: 23-May-1991

(viii) ATTORNEY/AGENT INFORMATION:
     (A) NAME: Hanson, Norman D.
     (B) REGISTRATION NUMBER: 30,946
     (C) REFERENCE/DOCKET NUMBER: LUD 253.3

(ix) TELECOMMUNICATION INFORMATION:
     (A) TELEPHONE: (212) 688-9200
     (B) TELEFAX: (212) 838-3884

(2)   INFORMATION FOR SEQUENCE ID NO: 1:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 462 base pairs
            (B) TYPE: nucleic acid
            (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: genomic DNA
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:


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CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG         180
CTTGTGAATT TGTACCCTTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC         240
CCCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT         300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG CATGCATTGT         360
GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT         420
TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CC                           462
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(2)   INFORMATION FOR SEQUENCE ID NO: 2:
       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 675 base pairs
           (B) TYPE: nucleic acid
           (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: genomic DNA
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:


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ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT        48
Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
                  5                  10                  15

GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA        96
Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
                 20                  25                  30

GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA       144
Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
             35                  40                  45

AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG       192
Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln
         50                  55                  60

TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC       240
Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser
65                  70                  75                  80

TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC       288
Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr
                 85                  90                  95

GAC GAC GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT       336
Asp Asp Glu Asp Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp
                100                 105                 110

GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA GAT GAG       384
Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu
                115                 120                 125

GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG       432
Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met
         130                 135                 140

GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG       480
Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys
145                 150                 155                 160

AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC       528
Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe
                 165                 170                 175
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CTG GTG TCT ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT        576
Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys
            180             185                 190

GAA AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG        624
Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu Glu
            195             200                 205

GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT        672
Glu Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro
210                 215                 220                 225

TAG                                                                    675
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(2)　INFORMATION FOR SEQUENCE ID NO: 3:
　　　(i) SEQUENCE CHARACTERISTICS:
　　　　　(A) LENGTH:　228 base pairs
　　　　　(B) TYPE:　nucleic acid
　　　　　(D) TOPOLOGY:　linear
　　　(ii) MOLECULE TYPE:　genomic DNA
　　　(xi) SEQUENCE DESCRIPTION:　SEQ ID NO: 3:


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GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG TTGTTTTTTT    60
TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA ATTTGATTTT GTTCTAAAGT   120
TCATTATGCA AAGATGTCAC CAACAGACTT CTGACTGCAT GGTGAACTTT CATATGATAC   180
ATAGGATTAC ACTTGTACCT GTTAAAAATA AAAGTTTGAC TTGCATAC              228
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(2)   INFORMATION FOR SEQUENCE ID NO: 4:
       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 1365 base pairs
           (B) TYPE: nucleic acid
           (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: genomic DNA
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:


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CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG           150
AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT           200
CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA           250
CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT           300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG           350
CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG           400
CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT           450
ACCCTTTGTG CC                                                    462
ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA          504
GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG          546
TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC          588
TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC          630
ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC          672
TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG          714
GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC          756
GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT          798
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA          840
GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA          882
GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT          924
GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT          966
TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG         1008
AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT         1050
GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG GAG GAG         1092
GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT         1134
TAG                                                             1137
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ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT          1287
CTGACTGCAT GGTGAACTTT CATATGATAC ATAGGATTAC ACTTGTACCT          1337
GTTAAAAATA AAAGTTTGAC TTGCATAC                                  1365
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(2)   INFORMATION FOR SEQUENCE ID NO: 5:
       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 4698 base pairs
            (B) TYPE: nucleic acid
            (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: genomic DNA
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:


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CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG         150
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CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA         250
CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT         300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG         350
CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG         400
CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT         450
ACCCTTTGTG CC                                                  462
ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA         504
GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG         546
TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC         588
TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC         630
ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC         672
TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG         714
GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC         756
GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT         798
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA         840
GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA         882
GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC T                  916
GTGAGTAACC CGTGGTCTTT ACTCTAGATT CAGGTGGGGT GCATTCTTTA         966
CTCTTGCCCA CATCTGTAGT AAAGACCACA TTTTGGTTGG GGGTCATTGC        1016
TGGAGCCATT CCTGGCTCTC CTGTCCACGC CTATCCCCGC TCCTCCCATC        1066
CCCCACTCCT TGCTCCGCTC TCTTTCCTTT TCCCACCTTG CCTCTGGAGC        1116
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TCCTGCTCCC CTCCCCCTCC CCTCCCTGTT TACCCTTCAC CGCTTTTCCT        1416
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CCTCCCCCTC TTTGCTCGAC TTTTAGCAGC CTTACCTCTC CCTGCTTTCT        1916
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AGCTCACCTT TTTGTTTGTT TGGTTGTTTG GTTGTTTGGT TTGCTTTTTT        2016
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CTTTTCTAGA CTCCCCCCTC CAGGCTTGCT GTTTGCTTCT GTGCACTTTT      2216
CCTGACCCTG CTCCCCTTCC CCTCCCAGCT CCCCCCTCTT TTCCCACCTC      2266
CCTTTCTCCA GCCTGTCACC CCTCCTTCTC TCCTCTCTGT TTCTCCCACT      2316
TCCTGCTTCC TTTACCCCTT CCCTCTCCCT ACTCTCCTCC CTGCCTGCTG      2366
GACTTCCTCT CCAGCCGCCC AGTTCCCTGC AGTCCTGGAG TCTTTCCTGC      2416
CTCTCTGTCC ATCACTTCCC CCTAGTTTCA CTTCCCTTTC ACTCTCCCCT      2466
ATGTGTCTCT CTTCCTATCT ATCCCTTCCT TTCTGTCCCC TCTCCTCTGT      2516
CCATCACCTC TCTCCTCCCT TCCCTTTCCT CTCTCTTCCA TTTTCTTCCA      2566
CCTGCTTCTT TACCCTGCCT CTCCCATTGC CCTCTTACCT TTATGCCCAT      2616
TCCATGTCCC CTCTCAATTC CCTGTCCCAT TGTGCTCCCT CACATCTTCC      2666
ATTTCCCTCT TTCTCCCTTA GCCTCTTCTT CCTCTTCTCT TGTATCTCCC      2716
TTCCCTTTGC TTCTCCCTCC TCCTTTCCCC TTCCCCTATG CCCTCTACTC      2766
TACTTGATCT TCTCTCCTCT CCACATACCC TTTTTCCTTT CCACCCTGCC      2816
CTTTGTCCCC AGACCCTACA GTATCCTGTG CACAGGAAGT GGGAGGTGCC      2866
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CAGGCCATGC TCCATGCTTG GCGCTTGCTC AGCGTGGTTA AGTAATGGGA      3116
GAATCTGAAA ACTAGGGGCC AGTGGTTTGT TTTGGGGACA AATTAGCACG      3166
TAGTGATATT TCCCCCTAAA AATTATAACA AACAGATTCA TGATTTGAGA      3216
TCCTTCTACA GGTGAGAAGT GGAAAAATTG TCACTATGAA GTTCTTTTTA      3266
GGCTAAAGAT ACTTGGAACC ATAGAAGCGT TGTTAAAATA CTGCTTTCTT      3316
TTGCTAAAAT ATTCTTTCTC ACATATTCAT ATTCTCCAG                  3355
 GT GTT CCT GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT     3396
AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT    3438
ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA    3480
AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA    3522
GAG GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC    3564
TTC TCA CCT TAG                                            3576
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GCTAAGAGCA TCTTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA      3676
TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA      3726
CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT      3776
GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA      3826
GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG      3876
TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT      3926
TTCAAGAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT TATTTTGTCG      3976
TTCTGATTTT TTTCATTTCT AGACCTGTGG TTTTAAAGAG ATGAAAATCT      4026
CTTAAAATTT CCTTCATCTT TAATTTTCCT TAACTTTAGT TTTTTTCACT      4076
TAGAATTCAA TTCAAATTCT TAATTCAATC TTAATTTTTA GATTTCTTAA      4126
AATGTTTTTT AAAAAAAATG CAAATCTCAT TTTTAAGAGA TGAAAGCAGA      4176
GTAACTGGGG GGCTTAGGGA ATCTGTAGGG TTGCGGTATA GCAATAGGGA      4226
GTTCTGGTCT CTGAGAAGCA GTCAGAGAGA ATGGAAAACC AGGCCCTTGC      4276
CAGTAGGTTA GTGAGGTTGA TATGATCAGA TTATGGACAC TCTCCAAATC      4326
ATAAATACTC TAACAGCTAA GGATCTCTGA GGGAAACACA ACAGGGAAAT      4376
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AGTCAGGAGT GTATTCTAAT AAGTGTTGCT TATCTCTTAT TTTCTTCTAC      4476
AGTTGCAAAG CCCAGAAGAA AGAAATGGAC AGCGGAAGAA GTGGTTGTTT      4526
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TTTTGTTCTA AAGTTCATTA TGCAAGATG TCACCAACAG ACTTCTGACT       4626
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GCATGGTGAA CTTTCATATG ATACATAGGA TTACACTTGT ACCTGTTAAA        4676
AATAAAAGTT TGACTTGCAT AC                                      4698
```

(2)   INFORMATION FOR SEQUENCE ID NO: 6:
       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 7 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: protein
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Leu Pro Tyr Leu Gly Trp Leu
                 5

(2)   INFORMATION FOR SEQUENCE ID NO: 7:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 2418 base pairs
           (B) TYPE: nucleic acid
           (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: genomic DNA
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:


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GGATCCAGGC CCTGCCAGGA AAAATATAAG GGCCCTGCGT GAGAACAGAG        50
GGGGTCATCC ACTGCATGAG AGTGGGGATG TCACAGAGTC CAGCCCACCC       100
TCCTGGTAGC ACTGAGAAGC CAGGGCTGTG CTTGCGGTCT GCACCCTGAG       150
GGCCCGTGGA TTCCTCTTCC TGGAGCTCCA GGAACCAGGC AGTGAGGCCT       200
TGGTCTGAGA CAGTATCCTC AGGTCACAGA GCAGAGGATG CACAGGGTGT       250
GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA       300
CAGGACACAT AGGACTCCAC AGAGTCTGGC CTCACCTCCC TACTGTCAGT       350
CCTGTAGAAT CGACCTCTGC TGGCCGGCTG TACCCTGAGT ACCCTCTCAC       400
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CTCTCCCCAG GCCTGTGGGT CTTCATTGCC CAGCTCCTGC CCACACTCCT       600
GCCTGCTGCC CTGACGAGAG TCATCATGTC TCTTGAGCAG AGGAGTCTGC       650
ACTGCAAGCC TGAGGAAGCC CTTGAGGCCC AACAAGAGGC CCTGGGCCTG       700
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CCTGGAGGAG GTGCCCACTG CTGGGTCAAC AGATCCTCCC CAGAGTCCTC       800
AGGGAGCCTC CGCCTTTCCC ACTACCATCA ACTTCACTCG ACAGAGGCAA       850
CCCAGTGAGG GTTCCAGCAG CCGTGAAGAG GAGGGGCCAA GCACCTCTTG       900
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TGGTTGGTTT TCTGCTCCTC AAATATCGAG CCAGGGAGCC AGTCACAAAG      1000
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GATCTTCGGC AAAGCCTCTG AGTCCTTGCA GCTGGTCTTT GGCATTGACG      1100
TGAAGGAAGC AGACCCCACC GGCCACTCCT ATGTCCTTGT CACCTGCCTA      1150
GGTCTCTCCT ATGATGGCCT GCTGGGTGAT AATCAGATCA TGCCCAAGAC      1200
AGGCTTCCTG ATAATTGTCC TGGTCATGAT TGCAATGGAG GGCGGCCATG      1250
CTCCTGAGGA GGAAATCTGG GAGGAGCTGA GTGTGATGGA GGTGTATGAT      1300
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TTCTTCCCAT CCCTGCGTGA AGCAGCTTTG AGAGAGGAGG AAGAGGGAGT      1550
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GTCTTGTGTT TTATTCAGAT TGGGAAATCC ATTCTATTTT GTGAATTGGG      1900
ATAATAACAG CAGTGGAATA AGTACTTAGA AATGTGAAAA ATGAGCAGTA      1950
AAATAGATGA GATAAAGAAC TAAAGAAATT AAGAGATAGT CAATTCTTGC      2000
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GGGTGTGGGG CTCCGGGTGA GAGTGGTGGA GTGTCAATGC CCTGAGCTGG          2350
GGCATTTTGG GCTTTGGGAA ACTGCAGTTC CTTCTGGGGG AGCTGATTGT          2400
AATGATCTTG GGTGGATCC                                            2418
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AGAATCCGGT TCCACCCCTG CTCTCAACCC AGGGAAGCCC AGGTGCCCAG       150
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CGGTCTGAGG GGCGGCTTGA GATCGGTGGA GGGAAGCGGG CCCAGCTCTG       250
TAAGGAGGCA AGGTGACATG CTGAGGGAGG ACTGAGGACC CACTTACCCC       300
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GGTGGACTTC TCAGGCTGGG CCACCCCCAG CCCCCTTGCT GCTTAAACCA       400
CTGGGGACTC GAAGTCAGAG CTCCGTGTGA TCAGGGAAGG GCTGCTTAGG       450
AGAGGGCAGC GTCCAGGCTC TGCCAGACAT CATGCTCAGG ATTCTCAAGG       500
AGGGCTGAGG GTCCCTAAGA CCCCACTCCC GTGACCCAAC CCCCACTCCA       550
ATGCTCACTC CCGTGACCCA ACCCCCTCTT CATTGTCATT CCAACCCCCA       600
CCCCACATCC CCCACCCCAT CCCTCAACCC TGATGCCCAT CCGCCCAGCC       650
ATTCCACCCT CACCCCCACC CCCACCCCCA CGCCCACTCC CACCCCCACC       700
CAGGCAGGAT CCGGTTCCCG CCAGGAAACA TCCGGGTGCC CGGATGTGAC       750
GCCACTGACT TGCGCATTGT GGGGCAGAGA GAAGCGAGGT TTCCATTCTG       800
AGGGACGGCG TAGAGTTCGG CCGAAGGAAC CTGACCCAGG CTCTGTGAGG       850
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GAGAGCCCCA AATATTCCAG CCCCGCCCTT GCTGCCAGCC CTGGCCCACC       950
CGCGGGAAGA CGTCTCAGCC TGGGCTGCCC CCAGACCCCT GCTCCAAAAG      1000
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CCCATCTCCT CAGCTACACC TCCACCCCCA TCCCTACTCC TACTCCGTCA      1250
CCTGACCACC ACCCTCCAGC CCCAGCACCA GCCCCAACCC TTCTGCCACC      1300
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ATCCACTGAG GGGAGTGGTT TTAGGCTCTG TGAGGAGGCA AGGTGAGATG      1550
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ATCCAGTACC ACCCCTGCTG CCAGCCCTGG ACCACCCGGC CAGGACAGAT      1650
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CACCGCCACC CCACTCACAT TCCCATACCT ACCCCCTACC CCCAACCTCA      1900
TCTTGTCAGA ATCCCTGCTG TCAACCCACG GAAGCCACGG GAATGGCGGC      1950
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GCTTGAACAG GGCCTCAGGG GAGCAGAGGG AGGGCCCTAC TGCGAGATGA      2050
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CAG GCT GCC ACC TCC TCC TCC TCT CCT CTG GTC CTG GGC ACC          4056
CTG GAG GAG GTG CCC ACT GCT GGG TCA ACA GAT CCT CCC CAG          4098
AGT CCT CAG GGA GCC TCC GCC TTT CCC ACT ACC ATC AAC TTC          4140
ACT CGA CAG AGG CAA CCC AGT GAG GGT TCC AGC AGC CGT GAA          4182
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CGA GCA GTA ATC ACT AAG AAG GTG GCT GAT TTG GTT GGT TTT          4266
CTG CTC CTC AAA TAT CGA GCC AGG GAG CCA GTC ACA AAG GCA          4308
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TTT GGC ATT GAC GTG AAG GAA GCA GAC CCC ACC GGC CAC TCC          4434
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(2)   INFORMATION FOR SEQUENCE ID NO: 9:
       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 4157 base pairs
            (B) TYPE: nucleic acid
            (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: genomic DNA
       (ix) FEATURE:
            (A) NAME/KEY: MAGE-2 gene
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:


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GCTCAGTCGC CACCACCTCA CCCCGCCACC CCCGCCGCT TTAACCGCAG         350
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TTC TCG ACT ACC ATC AAC TAC ACT CTT TGG AGA CAA TCC GAT         2849
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(2)   INFORMATION FOR SEQUENCE ID NO: 10:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 662 base pairs
            (B) TYPE: nucleic acid
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: genomic DNA
      (ix) FEATURE:
            (A) NAME/KEY: MAGE-21 gene
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

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(2) INFORMATION FOR SEQUENCE ID NO: 11:
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         (A) LENGTH: 1640 base pairs
         (B) TYPE: nucleic acid
         (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: cDNA to mRNA
    (ix) FEATURE:
         (A) NAME/KEY: cDNA MAGE-3
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:


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(2)   INFORMATION FOR SEQUENCE ID NO: 12:
       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 943 base pairs
           (B) TYPE: nucleic acid
           (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: genomic DNA
       (ix) FEATURE:
           (A) NAME/KEY: MAGE-31 gene
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:


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CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT         706
TCT AGT GTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC         748
GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC         790
CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT         832
GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC         874
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(2) INFORMATION FOR SEQUENCE ID NO: 13:
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          (A) LENGTH: 1067 base pairs
          (B) TYPE: nucleic acid
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA to mRNA
     (ix) FEATURE:
          (A) NAME/KEY: cDNA MAGE-4
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:


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    ATG CTG GAG AGA GTC ATC AAA AAT TAC AAG CGC TGC TTT CCT       165
    GTG ATC TTC GGC AAA GCC TCC GAG TCC CTG AAG ATG ATC TTT       207
    GGC ATT GAC GTG AAG GAA GTG GAC CCC GCC AGC AAC ACC TAC       249
    ACC CTT GTC ACC TGC CTG GGC CTT TCC TAT GAT GGC CTG CTG       291
    GGT AAT AAT CAG ATC TTT CCC AAG ACA GGC CTT CTG ATA ATC       333
    GTC CTG GGC ACA ATT GCA ATG GAG GGC GAC AGC GCC TCT GAG       375
    GAG GAA ATC TGG GAG GAG CTG GGT GTG ATG GGG GTG TAT GAT       417
    GGG AGG GAG CAC ACT GTC TAT GGG GAG CCC AGG AAA CTG CTC       459
    ACC CAA GAT TGG GTG CAG GAA AAC TAC CTG GAG TAC CGG CAG       501
    GTA CCC GGC AGT AAT CCT GCG CGC TAT GAG TTC CTG TGG GGT       543
    CCA AGG GCT CTG GCT GAA ACC AGC TAT GTG AAA GTC CTG GAG       585
    CAT GTG GTC AGG GTC AAT GCA AGA GTT CGC ATT GCC TAC CCA       627
    TCC CTG CGT GAA GCA GCT TTG TTA GAG GAG GAA GAG GGA GTC       669
    TGAGCATGAG TTGCAGCCAG GGCTGTGGGG AAGGGGCAGG GCTGGGCCAG       719
    TGCATCTAAC AGCCCTGTGC AGCAGCTTCC CTTGCCTCGT GTAACATGAG       769
    GCCCATTCTT CACTCTGTTT GAAGAAAATA GTCAGTGTTC TTAGTAGTGG       819
    GTTTCTATTT TGTTGGATGA CTTGGAGATT TATCTCTGTT TCCTTTTACA       869
    ATTGTTGAAA TGTTCCTTTT AATGGATGGT TGAATTAACT TCAGCATCCA       919
    AGTTTATGAA TCGTAGTTAA CGTATATTGC TGTTAATATA GTTTAGGAGT       969
    AAGAGTCTTG TTTTTTATTC AGATTGGGAA ATCCGTTCTA TTTTGTGAAT      1019
    TTGGGACATA ATAACAGCAG TGGAGTAAGT ATTTAGAAGT GTGAATTC       1067
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(2)   INFORMATION FOR SEQUENCE ID NO: 14:
      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 226 base pairs
          (B) TYPE: nucleic acid
          (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: genomic DNA
      (ix) FEATURE:
          (A) NAME/KEY: MAGE-5 gene
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:


```
AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG ATCTGTAAGT                50
AAGCCTTTGT TAGAGCCTCC AAGGTTCAGT TTTTAGCTGA GGCTTCTCAC               100
ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC AGCTCCTGCC               150
CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC                                184
ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA              226
```

(2)   INFORMATION FOR SEQUENCE ID NO: 15:
       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 225 base pairs
            (B) TYPE: nucleic acid
            (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: cDNA
       (ix) FEATURE:
            (A) NAME/KEY: MAGE-6 gene
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT TCC GAT TCC TTG   42
CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA GTG GAC CCC ATC   84
GGC CAC GTG TAC ATC TTT GCC ACC TGC CTG GGC CTC TCC TAC   126
GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG CCC AGG ACA GGC   168
TTC CTG ATA ATC ATC CTG GCC ATA ATC GCA AGA GAG GGC GAC   210
TGT GCC CCT GAG GAG   225

(2)   INFORMATION FOR SEQUENCE ID NO: 16:
       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 166 base pairs
           (B) TYPE: nucleic acid
           (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: genomic DNA
      (ix) FEATURE:
           (A) NAME/KEY: MAGE-7 gene
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:


```
ACA AGC ACT AGT TTC CTT GTG ATC TAT GGC AAA GCC TCA GAG          42
TGC ATG CAG GTG ATG TTT GGC ATT GAC ATG AAG GAA GTG GAC          84
CCC GCG GCC ACT CCT ACG TCT TGT ACC TGC TTG GGC CTC TCC          126
TAC AAT GGC CTG CTG GGT GAT GAT CAG AGC ATG CCC GAG A            166
```

(1) GENERAL INFORMATION:

   (i) APPLICANTS: Boon, Thierry, Van den Eynde, Benoît

   (ii) TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor Rejection Antigens and Uses Thereof

   (iii) NUMBER OF SEQUENCES: 16

   (iv) CORRESPONDENCE ADDRESS:
       (A) ADDRESSEE: Felfe & Lynch
       (B) STREET: 805 Third Avenue
       (C) CITY: New York City
       (D) STATE: New York
       (F) ZIP: 10022

   (v) COMPUTER READABLE FORM:
       (A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
       (B) COMPUTER: IBM
       (C) OPERATING SYSTEM: PC-DOS
       (D) SOFTWARE: Wordperfect

   (vi) CURRENT APPLICATION DATA:
       (A) APPLICATION NUMBER: 07/807,043
       (B) FILING DATE: 12-DECEMBER-1991
       (C) CLASSIFICATION:

   (vii) PRIOR APPLICATION DATA:
       (A) APPLICATION NUMBER: 07/764,364
       (B) FILING DATE: 23-SEPTEMBER-1991

   (vii) PRIOR APPLICATION DATA:
       (A) APPLICATION NUMBER: 07/728,838
       (B) FILING DATE: 9-JULY-1991

   (vii) PRIOR APPLICATION DATA:
       (A) APPLICATION NUMBER: 07/705,702
       (B) FILING DATE: 23-May-1991

   (viii) ATTORNEY/AGENT INFORMATION:
       (A) NAME: Hanson, Norman D.
       (B) REGISTRATION NUMBER: 30,946
       (C) REFERENCE/DOCKET NUMBER: LUD 253.3

   (ix) TELECOMMUNICATION INFORMATION:
       (A) TELEPHONE: (212) 688-9200
       (B) TELEFAX: (212) 838-3884

(2)   INFORMATION FOR SEQUENCE ID NO: 1:
      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 462 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: singular
          (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: genomic DNA
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:


```
ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG         60
ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT CAGCCAATGA GCTTACTGTT        120
CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG        180
CTTGTGAATT TGTACCCTTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC        240
CCCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT        300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG CATGCATTGT        360
GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT        420
TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CC                           462
```

(2) INFORMATION FOR SEQUENCE ID NO: 2:
     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 675 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: singular
         (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: genomic DNA
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:


```
ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT        48
Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
                  5                  10                  15

GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA        96
Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
                 20                  25                  30

GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA       144
Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
             35                  40                  45

AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG       192
Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln
         50                  55                  60

TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC       240
Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser
65                  70                  75                  80

TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC       288
Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr
                 85                  90                  95

GAC GAC GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT       336
Asp Asp Glu Asp Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp
                100                 105                 110

GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA GAT GAG       384
Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu
             115                 120                 125

GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG       432
Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met
         130                 135                 140

GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG       480
Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys
145                 150                 155                 160

AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC       528
Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe
                165                 170                 175
```

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CTG GTG TCT ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT       576
Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys
            180             185                 190

GAA AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG       624
Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu Glu
            195             200                 205

GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT       672
Glu Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro
210             215                 220                 225

TAG                                                                    675
```

(2)   INFORMATION FOR SEQUENCE ID NO: 3:
      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 228 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: singular
          (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: genomic DNA
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:


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GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG TTGTTTTTTT       60
TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA ATTTGATTTT GTTCTAAAGT      120
TCATTATGCA AAGATGTCAC CAACAGACTT CTGACTGCAT GGTGAACTTT CATATGATAC      180
ATAGGATTAC ACTTGTACCT GTTAAAAATA AAAGTTTGAC TTGCATAC                   228
```

(2)   INFORMATION FOR SEQUENCE ID NO: 4:
       (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 1365 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: singular
             (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: genomic DNA
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:


```
ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT          50
GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT         100
CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG         150
AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT         200
CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA         250
CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT         300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG         350
CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG         400
CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT         450
ACCCTTTGTG CC                                                 462
ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA       504
GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG       546
TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC       588
TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC       630
ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC       672
TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG       714
GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC       756
GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT       798
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA       840
GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA       882
GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT       924
GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT       966
TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG      1008
AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT      1050
GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG GAG GAG      1092
GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT      1134
TAG                                                         1137
GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG      1187
TTGTTTTTTT TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA      1237
ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT      1287
CTGACTGCAT GGTGAACTTT CATATGATAC ATAGGATTAC ACTTGTACCT      1337
GTTAAAAATA AAAGTTTGAC TTGCATAC                              1365
```

(2) INFORMATION FOR SEQUENCE ID NO: 5:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4698 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: singular
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: genomic DNA
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:


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ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT        50
GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT       100
CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG       150
AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT       200
CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA       250
CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT       300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG       350
CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG       400
CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT       450
ACCCTTTGTG CC                                                462
ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA       504
GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG       546
TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC       588
TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC       630
ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC       672
TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG       714
GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC       756
GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT       798
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA       840
GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA       882
GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC T                916
GTGAGTAACC CGTGGTCTTT ACTCTAGATT CAGGTGGGGT GCATTCTTTA       966
CTCTTGCCCA CATCTGTAGT AAAGACCACA TTTTGGTTGG GGGTCATTGC      1016
TGGAGCCATT CCTGGCTCTC CTGTCCACGC CTATCCCCGC TCCTCCCATC      1066
CCCCACTCCT TGCTCCGCTC TCTTTCCTTT TCCCACCTTG CCTCTGGAGC      1116
TTCAGTCCAT CCTGCTCTGC TCCCTTTCCC CTTTGCTCTC CTTGCTCCCC      1166
TCCCCCTCGG CTCAACTTTT CGTGCCTTCT GCTCTCTGAT CCCCACCCTC      1216
TTCAGGCTTC CCCATTTGCT CCTCTCCCGA AACCCTCCCC TTCCTGTTCC      1266
CCTTTTCGCG CCTTTTCTTT CCTGCTCCCC TCCCCCTCCC TATTTACCTT      1316
TCACCAGCTT TGCTCTCCCT GCTCCCCTCC CCCTTTTGCA CCTTTTCTTT      1366
TCCTGCTCCC CTCCCCCTCC CCTCCCTGTT TACCCTTCAC CGCTTTTCCT      1416
CTACCTGCTT CCCTCCCCCT TGCTGCTCCC TCCCTATTTG CATTTTCGGG      1466
TGCTCCTCCC TCCCCCTCCC CCTCCCTCCC TATTTGCATT TTCGGGTGCT      1516
CCTCCCTCCC CCTCCCCAGG CCTTTTTTTT TTTTTTTTTT TTTTTTTTTT      1566
TTGGTTTTTC GAGACAGGGT TTCTCTTTGT ATCCCTGGCT GTCCTGGCAC      1616
TCACTCTGTA GACCAGGCTG GCCTCAAACT CAGAAATCTG CCTGCCTCTG      1666
CCTCCCAAAT GCTGGGATTA AAGGCTTGCA CCAGGACTGC CCCAGTGCAG      1716
GCCTTTCTTT TTTCTCCTCT CTGGTCTCCC TAATCCCTTT TCTGCATGTT      1766
AACTCCCCTT TTGGCACCTT TCCTTTACAG GACCCCCTCC CCCTCCCTGT      1816
TTCCCTTCCG GCACCCTTCC TAGCCCTGCT CTGTTCCCTC TCCCTGCTCC      1866
CCTCCCCCTC TTTGCTCGAC TTTTAGCAGC CTTACCTCTC CCTGCTTTCT      1916
GCCCCGTTCC CCTTTTTTGT GCCTTTCCTC CTGGCTCCCC TCCACCTTCC      1966
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AGCTCACCTT TTTGTTTGTT TGGTTGTTTG GTTGTTTGGT TTGCTTTTTT        2016
TTTTTTTTTT GCACCTTGTT TTCCAAGATC CCCCTCCCCC TCCGGCTTCC        2066
CCTCTGTGTG CCTTTCCTGT TCCCTCCCCC TCGCTGGCTC CCCCTCCCTT        2116
TCTGCCTTTC CTGTCCCTGC TCCCTTCTCT GCTAACCTTT TAATGCCTTT        2166
CTTTTCTAGA CTCCCCCCTC CAGGCTTGCT GTTTGCTTCT GTGCACTTTT        2216
CCTGACCCTG CTCCCCTTCC CCTCCCAGCT CCCCCCTCTT TTCCCACCTC        2266
CCTTTCTCCA GCCTGTCACC CCTCCTTCTC TCCTCTCTGT TTCTCCCACT        2316
TCCTGCTTCC TTTACCCCTT CCCTCTCCCT ACTCTCCTCC CTGCCTGCTG        2366
GACTTCCTCT CCAGCCGCCC AGTTCCCTGC AGTCCTGGAG TCTTTCCTGC        2416
CTCTCTGTCC ATCACTTCCC CCTAGTTTCA CTTCCCTTTC ACTCTCCCCT        2466
ATGTGTCTCT CTTCCTATCT ATCCCTTCCT TTCTGTCCCC TCTCCTCTGT        2516
CCATCACCTC TCTCCTCCCT TCCCTTTCCT CTCTCTTCCA TTTTCTTCCA        2566
CCTGCTTCTT TACCCTGCCT CTCCCATTGC CCTCTTACCT TTATGCCCAT        2616
TCCATGTCCC CTCTCAATTC CCTGTCCCAT TGTGCTCCCT CACATCTTCC        2666
ATTTCCCTCT TTCTCCCTTA GCCTCTTCTT CCTCTTCTCT TGTATCTCCC        2716
TTCCCTTTGC TTCTCCCTCC TCCTTTCCCC TTCCCTATG CCCTCTACTC        2766
TACTTGATCT TCTCTCCTCT CCACATACCC TTTTTCCTTT CCACCCTGCC        2816
CTTTGTCCCC AGACCCTACA GTATCCTGTG CACAGGAAGT GGGAGGTGCC        2866
ATCAACAACA AGGAGGCAAG AAACAGAGCA AAATCCCAAA ATCAGCAGGA        2916
AAGGCTGGAT GAAAATAAGG CCAGGTTCTG AGGACAGCTG GAATCTAGCC        2966
AAGTGGCTCC TATAACCCTA AGTACCAAGG GAGAAAGTGA TGGTGAAGTT        3016
CTTGATCCTT GCTGCTTCTT TTACATATGT TGGCACATCT TTCTCAAATG        3066
CAGGCCATGC TCCATGCTTG GCGCTTGCTC AGCGTGGTTA AGTAATGGGA        3116
GAATCTGAAA ACTAGGGGCC AGTGGTTTGT TTTGGGGACA AATTAGCACG        3166
TAGTGATATT TCCCCCTAAA AATTATAACA AACAGATTCA TGATTTGAGA        3216
TCCTTCTACA GGTGAGAAGT GGAAAAATTG TCACTATGAA GTTCTTTTTA        3266
GGCTAAAGAT ACTTGGAACC ATAGAAGCGT TGTTAAAATA CTGCTTTCTT        3316
TTGCTAAAAT ATTCTTTCTC ACATATTCAT ATTCTCCAG                    3355
 GT GTT CCT GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT       3396
AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT       3438
ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA       3480
AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA       3522
GAG GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC       3564
TTC TCA CCT TAG                                               3576
GCATGCAGGT ACTGGCTTCA CTAACCAACC ATTCCTAACA TATGCCTGTA        3626
GCTAAGAGCA TCTTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA        3676
TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA        3726
CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT        3776
GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA        3826
GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG        3876
TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT        3926
TTCAAGAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT TATTTTGTCG        3976
TTCTGATTTT TTTCATTTCT AGACCTGTGG TTTTAAAGAG ATGAAAATCT        4026
CTTAAAATTT CCTTCATCTT TAATTTTCCT TAACTTTAGT TTTTTTCACT        4076
TAGAATTCAA TTCAAATTCT TAATTCAATC TTAATTTTTA GATTTCTTAA        4126
AATGTTTTTT AAAAAAAATG CAAATCTCAT TTTTAAGAGA TGAAAGCAGA        4176
GTAACTGGGG GGCTTAGGGA ATCTGTAGGG TTGCGGTATA GCAATAGGGA        4226
GTTCTGGTCT CTGAGAAGCA GTCAGAGAGA ATGGAAAACC AGGCCCTTGC        4276
CAGTAGGTTA GTGAGGTTGA TATGATCAGA TTATGGACAC TCTCCAAATC        4326
ATAAATACTC TAACAGCTAA GGATCTCTGA GGGAAACACA ACAGGGAAAT        4376
ATTTTAGTTT CTCCTTGAGA AACAATGACA AGACATAAAA TTGGCAAGAA        4426
AGTCAGGAGT GTATTCTAAT AAGTGTTGCT TATCTCTTAT TTTCTTCTAC        4476
AGTTGCAAAG CCCAGAAGAA AGAAATGGAC AGCGGAAGAA GTGGTTGTTT        4526
TTTTTTCCCC TTCATTAATT TTCTAGTTTT TAGTAATCCA GAAAATTTGA        4576
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TTTTGTTCTA AAGTTCATTA TGCAAAGATG TCACCAACAG ACTTCTGACT      4626
GCATGGTGAA CTTTCATATG ATACATAGGA TTACACTTGT ACCTGTTAAA      4676
AATAAAAGTT TGACTTGCAT AC                                    4698
```

(2)   INFORMATION FOR SEQUENCE ID NO: 6:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 7 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: singular
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: protein
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Leu Pro Tyr Leu Gly Trp Leu
                  5

(2)   INFORMATION FOR SEQUENCE ID NO: 7:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 2419 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: singular
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: genomic DNA
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:


```
GGATCCAGGC CCTGCCAGGA AAAATATAAG GGCCCTGCGT GAGAACAGAG          50
GGGGTCATCC ACTGCATGAG AGTGGGGATG TCACAGAGTC CAGCCCACCC         100
TCCTGGTAGC ACTGAGAAGC CAGGGCTGTG CTTGCGGTCT GCACCCTGAG         150
GGCCCGTGGA TTCCTCTTCC TGGAGCTCCA GGAACCAGGC AGTGAGGCCT         200
TGGTCTGAGA CAGTATCCTC AGGTCACAGA GCAGAGGATG CACAGGGTGT         250
GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA         300
CAGGACACAT AGGACTCCAC AGAGTCTGGC CTCACCTCCC TACTGTCAGT         350
CCTGTAGAAT CGACCTCTGC TGGCCGGCTG TACCCTGAGT ACCCTCTCAC         400
TTCCTCCTTC AGGTTTTCAG GGGACAGGCC AACCCAGAGG ACAGGATTCC         450
CTGGAGGCCA CAGAGGAGCA CCAAGGAGAA GATCTGTAAG TAGGCCTTTG         500
TTAGAGTCTC CAAGGTTCAG TTCTCAGCTG AGGCCTCTCA CACACTCCCT         550
CTCTCCCCAG GCCTGTGGGT CTTCATTGCC CAGCTCCTGC CCACACTCCT         600
GCCTGCTGCC CTGACGAGAG TCATCATGTC TCTTGAGCAG AGGAGTCTGC         650
ACTGCAAGCC TGAGGAAGCC CTTGAGGCCC AACAAGAGGC CCTGGGCCTG         700
GTGTGTGTGC AGGCTGCCAC CTCCTCCTCC TCTCCTCTGG TCCTGGGCAC         750
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TGGTTGGTTT TCTGCTCCTC AAATATGAG CCAGGGAGCC AGTCACAAAG        1000
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GATCTTCGGC AAAGCCTCTG AGTCCTTGCA GCTGGTCTTT GGCATTGACG        1100
TGAAGGAAGC AGACCCCACC GGCCACTCCT ATGTCCTTGT CACCTGCCTA        1150
GGTCTCTCCT ATGATGGCCT GCTGGGTGAT AATCAGATCA TGCCCAAGAC        1200
AGGCTTCCTG ATAATTGTCC TGGTCATGAT TGCAATGGAG GGCGGCCATG        1250
CTCCTGAGGA GGAAATCTGG GAGGAGCTGA GTGTGATGGA GGTGTATGAT        1300
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(2)   INFORMATION FOR SEQUENCE ID NO: 9:
       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 4157 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: singular
           (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: genomic DNA
       (ix) FEATURE:
           (A) NAME/KEY: MAGE-2 gene
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:


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(2)   INFORMATION FOR SEQUENCE ID NO: 10:
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            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: singular
            (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: genomic DNA
       (ix) FEATURE:
            (A) NAME/KEY: MAGE-21 gene
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

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(2)   INFORMATION FOR SEQUENCE ID NO: 11:
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             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: singular
             (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: cDNA to mRNA
       (ix) FEATURE:
             (A) NAME/KEY: cDNA MAGE-3
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:


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GTG GAC CCC ATC GGC CAC TTG TAC ATC TTT GCC ACC TGC CTG            717
GGC CTC TCC TAC GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG            759
CCC AAG GCA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA            801
AGA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG            843
CTG AGT GTG TTA GAG GTG TTT GAG GGG AGG GAA GAC AGT ATG            885
TTG GGG GAT CCC AAG AAG CTG CTC ACC CAA CAT TTC GTG CAG            927
GAA AAC TAC CTG GAG TAC CGG CAG GTC CCC GGC AGT GAT CCT            969
GCA TGT TAT GAA TTC CTG TGG GGT CCA AGG GCC CTC GTT GAA           1011
ACC AGC TAT GTG AAA GTC CTG CAC CAT ATG GTA AAG ATC AGT           1053
GGA GGA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAG TGG GTT           1095
TTG AGA GAG GGG GAA GAG TGA                                       1116
GTCTGAGCAC GAGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT           1166
GCACCTTCCG GGGCCGCATC CCTTAGTTTC CACTGCCTCC TGTGACGTGA           1216
GGCCCATTCT TCACTCTTTG AAGCGAGCAG TCAGCATTCT TAGTAGTGGG           1266
TTTCTGTTCT GTTGGATGAC TTTGAGATTA TTCTTTGTTT CCTGTTGGAG           1316
TTGTTCAAAT GTTCCTTTTA ACGGATGGTT GAATGAGCGT CAGCATCCAG           1366
GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGAG           1416
TAAGAGTCTT GttTTTTACT CAAATTgGGA AATCCATTCC ATTTTGTGAA           1466
TTGTGACATA ATAATAGCAG TGGTAAAAGT ATTTGCTTAA AATTGTGAGC           1516
GAATTAGCAA TAACATACAT GAGATAACTC AAGAAATCAA AAGATAGTTG           1566
ATTCTTGCCT TGTACCTCAA TCTATTCTGT AAAATTAAAC AAATATGCAA           1616
ACCAGGATTT CCTTGACTTC TTTG                                        1640
```

(2)   INFORMATION FOR SEQUENCE ID NO: 12:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 943 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: singular
           (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: genomic DNA
      (ix) FEATURE:
           (A) NAME/KEY: MAGE-31 gene
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:


```
GGATCCTCCA CCCCAGTAGA GTGGGGACCT CACAGAGTCT GGCCAACCCT          50
CCTGACAGTT CTGGGAATCC GTGGCTGCGT TTGCTGTCTG CACATTGGGG         100
GCCCGTGGAT TCCTCTCCCA GGAATCAGGA GCTCCAGGAA CAAGGCAGTG         150
AGGACTTGGT CTGAGGCAGT GTCCTCAGGT CACAGAGTAG AGGGGgCTCA         200
GATAGTGCCA ACGGTGAAGG TTTGCCTTGG ATTCAAACCA AGGGCCCCAC         250
CTGCCCCAGA ACACATGGAC TCCAGAGCGC CTGGCCTCAC CCTCAATACT         300
TTCAGTCCTG CAGCCTCAGC ATGCGCTGGC CGGATGTACC CTGAGGTGCC         350
CTCTCACTTC CTCCTTCAGG TTCTGAGGGG ACAGGCTGAC CTGGAGGACC         400
AGAGGCCCCC GGAGGAGCAC TGAAGGAGAA GATCTGTAAG TAAGCCTTTG         450
TTAGAGCCTC CAAGGTTCCA TTCAGTACTC AGCTGAGGTC TCTCACATGC         500
TCCCTCTCTC CCCAGGCCAG TGGGTCTCCA TTGCCCAGCT CCTGCCCACA         550
CTCCCGCCTG TTGCCCTGAC CAGAGTCATC                               580
ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA         622
GGC CTT GAG GCC CGA GGA GAg GCC CTG GGC CTG GTG GGT GCG         664
CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT         706
TCT AGT GTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC         748
GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC         790
CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT         832
GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC         874
CCT GAC CTG GAG TCT GAG TTC CAA GCA GCA CTC AGT AGG AAG         916
GTG GCC AAG TTG GTT CAT TTT CTG CTC                            943
```

(2) INFORMATION FOR SEQUENCE ID NO: 13:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1067 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: singular
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA to mRNA
     (ix) FEATURE:
          (A) NAME/KEY: cDNA MAGE-4
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:


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    GGG CCA AGC ACC TCG CCT GAC GCA GAG TCC TTG TTC CGA          39
GAA GCA CTC AGT AAC AAG GTG GAT GAG TTG GCT CAT TTT CTG          81
CTC CGC AAG TAT CGA GCC AAG GAG CTG GTC ACA AAG GCA GAA         123
ATG CTG GAG AGA GTC ATC AAA AAT TAC AAG CGC TGC TTT CCT         165
GTG ATC TTC GGC AAA GCC TCC GAG TCC CTG AAG ATG ATC TTT         207
GGC ATT GAC GTG AAG GAA GTG GAC CCC GCC AGC AAC ACC TAC         249
ACC CTT GTC ACC TGC CTG GGC CTT TCC TAT GAT GGC CTG CTG         291
GGT AAT AAT CAG ATC TTT CCC AAG ACA GGC CTT CTG ATA ATC         333
GTC CTG GGC ACA ATT GCA ATG GAG GGC GAC AGC GCC TCT GAG         375
GAG GAA ATC TGG GAG GAG CTG GGT GTG ATG GGG GTG TAT GAT         417
GGG AGG GAG CAC ACT GTC TAT GGG GAG CCC AGG AAA CTG CTC         459
ACC CAA GAT TGG GTG CAG GAA AAC TAC CTG GAG TAC CGG CAG         501
GTA CCC GGC AGT AAT CCT GCG CGC TAT GAG TTC CTG TGG GGT         543
CCA AGG GCT CTG GCT GAA ACC AGC TAT GTG AAA GTC CTG GAG         585
CAT GTG GTC AGG GTC AAT GCA AGA GTT CGC ATT GCC TAC CCA         627
TCC CTG CGT GAA GCA GCT TTG TTA GAG GAG GAA GAG GGA GTC         669
TGAGCATGAG TTGCAGCCAG GGCTGTGGGG AAGGGGCAGG GCTGGGCCAG         719
TGCATCTAAC AGCCCTGTGC AGCAGCTTCC CTTGCCTCGT GTAACATGAG         769
GCCCATTCTT CACTCTGTTT GAAGAAAATA GTCAGTGTTC TTAGTAGTGG         819
GTTTCTATTT TGTTGGATGA CTTGGAGATT TATCTCTGTT TCCTTTTACA         869
ATTGTTGAAA TGTTCCTTTT AATGGATGGT TGAATTAACT TCAGCATCCA         919
AGTTTATGAA TCGTAGTTAA CGTATATTGC TGTTAATATA GTTTAGGAGT         969
AAGAGTCTTG TTTTTTATTC AGATTGGGAA ATCCGTTCTA TTTTGTGAAT        1019
TTGGGACATA ATAACAGCAG TGGAGTAAGT ATTTAGAAGT GTGAATTC         1067
```

(2)   INFORMATION FOR SEQUENCE ID NO: 14:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 226 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: singular
            (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: genomic DNA
        (ix) FEATURE:
            (A) NAME/KEY: MAGE-5 gene
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:


```
AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG ATCTGTAAGT          50
AAGCCTTTGT TAGAGCCTCC AAGGTTCAGT TTTTAGCTGA GGCTTCTCAC          100
ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC AGCTCCTGCC          150
CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC                           184
ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA          226
```

(2) INFORMATION FOR SEQUENCE ID NO: 15:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 225 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: singular
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: cDNA
    (ix) FEATURE:
        (A) NAME/KEY: MAGE-6 gene
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:


```
TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT TCC GAT TCC TTG        42
CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA GTG GAC CCC ATC        84
GGC CAC GTG TAC ATC TTT GCC ACC TGC CTG GGC CTC TCC TAC       126
GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG CCC AGG ACA GGC       168
TTC CTG ATA ATC ATC CTG GCC ATA ATC GCA AGA GAG GGC GAC       210
TGT GCC CCT GAG GAG                                            225
```

(2)   INFORMATION FOR SEQUENCE ID NO: 16:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 166 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: singular
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: genomic DNA
    (ix) FEATURE:
        (A) NAME/KEY: MAGE-7 gene
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ACA AGC ACT AGT TTC CTT GTG ATC TAT GGC AAA GCC TCA GAG   42
TGC ATG CAG GTG ATG TTT GGC ATT GAC ATG AAG GAA GTG GAC   84
CCC GCG GCC ACT CCT ACG TCT TGT ACC TGC TTG GGC CTC TCC   126
TAC AAT GGC CTG CTG GGT GAT GAT CAG AGC ATG CCC GAG A   166